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## SEQUENCE LISTING

&lt;110&gt; Hepgenics Pty Ltd

&lt;120&gt; Viral Vector

&lt;130&gt; 12437050/EJH

&lt;150&gt; AU 2003901876

&lt;151&gt; 2003-04-17

&lt;160&gt; 13

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; duck

&lt;400&gt; 1

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&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 2

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&lt;210&gt; 3

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 3

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34

&lt;210&gt; 4

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; human

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34

&lt;210&gt; 5

&lt;211&gt; 3021

&lt;212&gt; DNA

&lt;213&gt; duck

&lt;400&gt; 5

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&lt;210&gt; 6

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; duck

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(984)

&lt;400&gt; 6

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Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly
1 5 10 15

gga gaa ata ctg tta aac caa ctt gcc gga agg atg atc cca aaa ggg 96
Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly
20 25 30

act ttg aca tgg tca ggc aag ttt cca aca cta gat cac gtg tta gac 144

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- 5 -

Thr	Leu	Thr	Trp	Ser	Gly	Lys	Phe	Pro	Thr	Leu	Asp	His	Val	Leu	Asp	
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cat	gtg	caa	aca	atg	gag	gag	ata	aac	acc	ctc	cag	aat	cag	gga	gct	192
His	Val	Gln	Thr	Met	Glu	Glu	Ile	Asn	Thr	Leu	Gln	Asn	Gln	Gly	Ala	
	50					55				60						
tgg	cct	gct	ggg	gcg	gga	agg	aga	gta	gga	tta	tca	aat	ccg	act	cct	240
Trp	Pro	Ala	Gly	Ala	Gly	Arg	Arg	Val	Gly	Leu	Ser	Asn	Pro	Thr	Pro	
	65			70					75						80	
caa	gag	att	cct	cag	ccc	cag	tgg	act	ccc	gag	gaa	gac	caa	aaa	gca	288
Gln	Glu	Ile	Pro	Gln	Pro	Gln	Trp	Thr	Pro	Glu	Glu	Asp	Gln	Lys	Ala	
				85					90					95		
cgc	gaa	gct	ttt	cgc	cgt	tat	caa	gaa	gaa	aga	cca	ccg	gaa	acc	acc	336
Arg	Glu	Ala	Phe	Arg	Arg	Tyr	Gln	Glu	Glu	Arg	Pro	Pro	Glu	Thr	Thr	
			100				105						110			
acc	att	cct	ccg	tct	tcc	cct	cct	cag	tgg	aag	cta	caa	ccc	ggg	gac	384
Thr	Ile	Pro	Pro	Ser	Ser	Pro	Pro	Gln	Trp	Lys	Leu	Gln	Pro	Gly	Asp	
		115					120					125				
gat	cca	ctc	ctg	gga	aat	cag	tct	ctc	ctc	gag	act	cat	ccg	cta	tac	432
Asp	Pro	Leu	Leu	Gly	Asn	Gln	Ser	Leu	Leu	Glu	Thr	His	Pro	Leu	Tyr	
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cag	tca	gaa	cca	gcg	gtg	cca	gtg	ata	aaa	act	ccc	ccc	ttg	aag	aag	480
Gln	Ser	Glu	Pro	Ala	Val	Pro	Val	Ile	Lys	Thr	Pro	Pro	Leu	Lys	Lys	
	145				150					155					160	
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Lys	Met	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	Ala	Gly	Leu	Ile	Gly	Leu	
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ctg	gta	agc	ttt	ttc	ttg	ttg	ata	aaa	att	cta	gaa	ata	ctg	agg	agg	576
Leu	Val	Ser	Phe	Phe	Leu	Leu	Ile	Lys	Ile	Leu	Glu	Ile	Leu	Arg	Arg	
			180					185					190			
cta	gat	tgg	tgg	tgg	att	tct	ctc	agt	tct	cca	aag	gga	aaa	atg	caa	624
Leu	Asp	Trp	Trp	Trp	Ile	Ser	Leu	Ser	Ser	Pro	Lys	Gly	Lys	Met	Gln	
		195					200					205				
tgc	gct	ttc	caa	gat	act	gga	gcc	caa	atc	tct	cca	cat	tac	gta	gga	672
Cys	Ala	Phe	Gln	Asp	Thr	Gly	Ala	Gln	Ile	Ser	Pro	His	Tyr	Val	Gly	
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Ser	Cys	Pro	Trp	Gly	Cys	Pro	Gly	Phe	Leu	Trp	Thr	Tyr	Leu	Arg	Leu	
	225				230					235					240	
ttt	atc	atc	ttc	ctc	tta	atc	ctg	cta	gta	gca	gca	ggc	ttg	ctg	tat	768
Phe	Ile	Ile	Phe	Leu	Leu	Ile	Leu	Leu	Val	Ala	Ala	Gly	Leu	Leu	Tyr	
				245					250					255		
ctg	acg	gac	aac	ggg	tct	act	att	tta	gga	aag	ctc	caa	tgg	gcg	tcg	816
Leu	Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser	

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260	265	270	
gtc tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg			864
Val Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro			
275	280	285	
aaa tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act			912
Lys Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr			
290	295	300	
tcc tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg			960
Ser Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr			
305	310	315	320
ctg tct gct ctt ttt tac aag agt			984
Leu Ser Ala Leu Phe Tyr Lys Ser			
325			

&lt;210&gt; 7

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; duck

&lt;400&gt; 7

Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly	
1 5 10 15	
Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly	
20 25 30	
Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp	
35 40 45	
His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala	
50 55 60	
Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro	
65 70 75 80	
Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala	
85 90 95	
Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr	
100 105 110	

- 7 -

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp  
 115 120 125

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr  
 130 135 140

Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys  
 145 150 155 160

Lys Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu  
 165 170 175

Leu Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg  
 180 185 190

Leu Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln  
 195 200 205

Cys Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly  
 210 215 220

Ser Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu  
 225 230 235 240

Phe Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr  
 245 250 255

Leu Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser  
 260 265 270

Val Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro  
 275 280 285

Lys Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr  
 290 295 300

Ser Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr  
 305 310 315 320

Leu Ser Ala Leu Phe Tyr Lys Ser  
 325

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&lt;210&gt; 8

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; duck

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(501)

&lt;400&gt; 8

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Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu	
1 5 10 15	

gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta	96
Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu	
20 25 30	

gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc	144
Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys	
35 40 45	

gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct	192
Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser	
50 55 60	

tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt	240
Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe	
65 70 75 80	

atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg	288
Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu	
85 90 95	

acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc	336
Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val	
100 105 110	

tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg aaa	384
Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys	
115 120 125	

tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act tcc	432
Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser	
130 135 140	

tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg ctg	480
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- 9 -

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu  
 145 150 155 160

tct gct ctt ttt tac aag agt  
 Ser Ala Leu Phe Tyr Lys Ser  
 165

501

&lt;210&gt; 9

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; duck

&lt;400&gt; 9

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Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu  
 20 25 30

Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys  
 35 40 45

Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser  
 50 55 60

Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe  
 65 70 75 80

Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu  
 85 90 95

Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val  
 100 105 110

Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys  
 115 120 125

Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser  
 130 135 140

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu

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145	150	155	160	
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Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly				
20 25 30				
act ttg aca tgg tca ggc aag ttt cca aca cta gat cac gtg tta gac				144
Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp				
35 40 45				
cat gtg caa aca atg gag gag ata aac acc ctc cag aat cag gga gct				192
His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala				
50 55 60				
tgg cct gct ggg gcg gga agg aga gta gga tta tca aat ccg act cct				240
Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro				
65 70 75 80				
caa gag att cct cag ccc cag tgg act ccc gag gaa gac caa aaa gca				288
Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala				
85 90 95				
cgc gaa gct ttt cgc cgt tat caa gaa gaa aga cca ccg gaa acc acc				336
Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr				
100 105 110				
acc att cct ccg tct tcc cct cct cag tgg aag cta caa ccc ggg gac				384
Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp				
115 120 125				

- 11 -

gat cca ctc ctg gga aat cag tct ctc ctc gag act cat ccg cta tac 432  
 Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr  
 130 135 140

cag tca gaa cca gcg gtg cca gtg ata aaa act ccc ccc ttg aag aag 480  
 Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys  
 145 150 155 160

aaa 483  
 Lys

<210> 11

<211> 161

<212> PRT

<213> duck

<400> 11

Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly  
 1 5 10 15

Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly  
 20 25 30

Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp  
 35 40 45

His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala  
 50 55 60

Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro  
 65 70 75 80

Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala  
 85 90 95

Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr  
 100 105 110

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp  
 115 120 125

- 12 -

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr  
 130 135 140

Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys  
 145 150 155 160

Lys

&lt;210&gt; 12

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; duck

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (501)

&lt;400&gt; 12

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 1 5 10 15

gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta 96  
 Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu  
 20 25 30

gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc 144  
 Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys  
 35 40 45

gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct 192  
 Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser  
 50 55 60

tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt 240  
 Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe  
 65 70 75 80

atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg 288  
 Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu  
 85 90 95

acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc 336

- 13 -

Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser	Val		
			100					105					110				
tca	gcc	ctt	ttc	tcc	tcc	atc	tct	tca	cta	ctg	ccc	tcg	gat	ccg	aaa		384
Ser	Ala	Leu	Phe	Ser	Ser	Ile	Ser	Ser	Leu	Leu	Pro	Ser	Asp	Pro	Lys		
		115					120				125						
tct	ctc	gtc	gct	tta	acg	ttt	gga	ctt	tca	ctt	ata	tgg	atg	act	tcc		432
Ser	Leu	Val	Ala	Leu	Thr	Phe	Gly	Leu	Ser	Leu	Ile	Trp	Met	Thr	Ser		
		130				135					140						
tcc	tct	gcc	acc	caa	acg	ctc	gtc	acc	tta	acg	caa	tta	gcc	acg	ctg		480
Ser	Ser	Ala	Thr	Gln	Thr	Leu	Val	Thr	Leu	Thr	Gln	Leu	Ala	Thr	Leu		
145					150				155						160		
tct	gct	ctt	ttt	tac	aag	agt											501
Ser	Ala	Leu	Phe	Tyr	Lys	Ser											
				165													

&lt;210&gt; 13

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; duck

&lt;400&gt; 13

Met	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	Ala	Gly	Leu	Ile	Gly	Leu	Leu		
1				5					10					15			

Val	Ser	Phe	Phe	Leu	Leu	Ile	Lys	Ile	Leu	Glu	Ile	Leu	Arg	Arg	Leu		
			20				25						30				

Asp	Trp	Trp	Trp	Ile	Ser	Leu	Ser	Ser	Pro	Lys	Gly	Lys	Met	Gln	Cys		
		35					40					45					

Ala	Phe	Gln	Asp	Thr	Gly	Ala	Gln	Ile	Ser	Pro	His	Tyr	Val	Gly	Ser		
	50					55					60						

Cys	Pro	Trp	Gly	Cys	Pro	Gly	Phe	Leu	Trp	Thr	Tyr	Leu	Arg	Leu	Phe		
65					70					75					80		

Ile	Ile	Phe	Leu	Leu	Ile	Leu	Leu	Val	Ala	Ala	Gly	Leu	Leu	Tyr	Leu		
				85					90					95			

Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser	Val		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

100

105

110

Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser  
130 135 140

Ser	Ser	Ala	Thr	Gln	Thr	Leu	Val	Thr	Leu	Thr	Gln	Leu	Ala	Thr	Leu
145					150					155					160

Ser Ala Leu Phe Tyr Lys Ser  
165